

SEQUENCE LISTING

<110> COSSON, BERTRAND
 PAILLARD, LUC
 LEGAGNEUX, VINCENT
 OSBORNE, HOWARD

<120> PEPTIDE PROTEIN TRANSLATION INHIBITOR AND THE USE
 THEREOF FOR PROTEIN TRANSLATION CONTROL

<130> 0510-1133

<140> 10/565,438

<141> 2006-01-20

<150> PCT/FR04/050345

<151> 2004-07-20

<160> 17

<170> PatentIn Ver. 3.3

<210> 1

<211> 28

<212> PRT

<213> *Xenopus laevis*

<400> 1

Val	Lys	Phe	Ala	Asp	Thr	Gln	Lys	Asp	Lys	Glu	Gln	Lys	Arg	Met	Thr
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Gln	Gln	Leu	Gln	Gln	Gln	Met	Gln	Gln	Leu	Asn	Ala
		20					25				

<210> 2

<211> 28

<212> PRT

<213> *Homo sapiens*

<400> 2

Val	Lys	Phe	Ala	Asp	Thr	Gln	Lys	Asp	Lys	Glu	Gln	Lys	Arg	Met	Ala
1				5				10						15	

Gln	Gln	Leu	Gln	Gln	Gln	Met	Gln	Gln	Ile	Ser	Ala
		20					25				

<210> 3

<211> 84

<212> PRT

<213> *Xenopus laevis*

<400> 3

Phe	Thr	Thr	Arg	Ser	Met	Ala	Gln	Met	Ala	Ile	Lys	Ser	Met	His	Gln
1				5				10						15	

Ala Gln Thr Met Glu Gly Cys Ser Ser Pro Ile Val Val Lys Phe Ala
 20 25 30
 Asp Thr Gln Lys Asp Lys Glu Gln Lys Arg Met Thr Gln Gln Leu Gln
 35 40 45
 Gln Gln Met Gln Gln Leu Asn Ala Ala Ser Met Trp Gly Asn Leu Thr
 50 55 60
 Gly Leu Asn Ser Leu Ala Pro Gln Tyr Leu Ala Leu Leu Gln Gln Thr
 65 70 75 80
 Ala Ser Ser Gly

<210> 4
 <211> 88
 <212> PRT
 <213> Homo sapiens

<400> 4
 Phe Thr Thr Arg Ala Met Ala Gln Thr Ala Ile Lys Ala Met His Gln
 1 5 10 15
 Ala Gln Thr Met Glu Gly Cys Ser Ser Pro Met Val Val Lys Phe Ala
 20 25 30
 Asp Thr Gln Lys Asp Lys Glu Gln Lys Arg Met Ala Gln Gln Leu Gln
 35 40 45
 Gln Gln Met Gln Gln Ile Ser Ala Ala Ser Val Trp Gly Asn Leu Ala
 50 55 60
 Gly Leu Asn Thr Leu Gly Pro Gln Tyr Leu Ala Leu Tyr Leu Gln Leu
 65 70 75 80
 Leu Gln Gln Thr Ala Ser Ser Gly
 85

<210> 5
 <211> 189
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 fusion protein

<400> 5
 Met Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Val Lys Phe Ala
 1 5 10 15
 Asp Thr Gln Lys Asp Lys Glu Gln Lys Arg Met Thr Gln Gln Leu Gln
 20 25 30

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<210> 6
<211> 154
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      fusion protein
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<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic fusion protein

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
1 5 10 15

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
35 40 45

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
50 55 60

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Glu Glu Leu Pro Val
65 70 75 80

Ala Gly Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
85 90 95

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
 100 105 110

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
 115 120 125

Ile Tyr Gly Gly Gly Gly Gly Ser Lys Leu Gly Ser Met Ala Tyr Pro
 130 135 140

Tyr Asp Val Pro Asp Tyr Ala Arg Ala Ala
 145 150

<210> 7
 <211> 570
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 fusion polynucleotide

<400> 7
 atggcttacc catac gatgt tccagattac gctagcgtaa agttcgcaga cactcagaaa 60
 gacaaagaac agaagcgc at gacgcagcaa cttcagcagc aaatgcagca gctcaatgca 120
 gcggccgccca tggcttctaa ctttactcag ttcggttctcg tcgacaatgg cggaactggc 180
 gacgtgactg tcgccccaa g caacttcgct aacgggggtcg ctgaatggat cagctctaac 240
 tcgcgatcac aggccttaca agtaacctgt agcggttcgtc agagctctgc gcagaatcgc 300
 aaatacacca tcaaagtcga ggtgcctaaa gtggcaaccc agactggttg tgggaagag 360
 cttcctgtag ccggatggag atcttactta aatatggaac taaccattcc aattttcgcc 420
 acgaattccg actgcgagct tattgttaag gcaatgcaag gtctcctaaa agatggaaac 480
 ccgattccct cggccatcgc ggccaactcc ggcatctacg gaggtggagg tggatctggg 540
 ccctattcta tagtgcacc taaatgctag 570

<210> 8
 <211> 570
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 fusion polynucleotide

<400> 8
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 gacaaagaac agaagagaat ggcccagcag cttcagcagc agatgcagca aatcagcgca 120
 gcggccgccca tggcttctaa ctttactcag ttcggttctcg tcgacaatgg cggaactggc 180
 gacgtgactg tcgccccaa g caacttcgct aacgggggtcg ctgaatggat cagctctaac 240
 tcgcgatcac aggccttaca agtaacctgt agcggttcgtc agagctctgc gcagaatcgc 300
 aaatacacca tcaaagtcga ggtgcctaaa gtggcaaccc agactggttg tgggaagag 360
 cttcctgtag ccggatggag atcttactta aatatggaac taaccattcc aattttcgcc 420
 acgaattccg actgcgagct tattgttaag gcaatgcaag gtctcctaaa agatggaaac 480
 ccgattccct cggccatcgc ggccaactcc ggcatctacg gaggtggagg tggatctggg 540
 ccctattcta tagtgcacc taaatgctag 570

<210> 9
 <211> 489
 <212> PRT
 <213> Xenopus laevis

<400> 9
 Met Asn Gly Thr Met Asp His Pro Asp His Pro Asp Pro Asp Ser Ile
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 Lys Met Phe Val Gly Gln Val Pro Arg Ser Trp Ser Glu Lys Glu Leu
 20 25 30
 Arg Glu Leu Phe Glu Gln Tyr Gly Ala Val Tyr Glu Ile Asn Val Leu
 35 40 45
 Arg Asp Arg Ser Gln Asn Pro Pro Gln Ser Lys Gly Cys Cys Phe Ile
 50 55 60
 Thr Phe Tyr Thr Arg Lys Ala Ala Leu Glu Ala Gln Asn Ala Leu His
 65 70 75 80
 Asn Met Lys Val Leu Pro Gly Met His His Pro Ile Gln Met Lys Pro
 85 90 95
 Ala Asp Ser Glu Lys Asn Asn Ala Val Glu Asp Arg Lys Leu Phe Ile
 100 105 110
 Gly Met Val Ser Lys Asn Cys Asn Glu Asn Asp Ile Arg Ala Met Phe
 115 120 125
 Ser Pro Phe Gly Gln Ile Glu Glu Cys Arg Ile Leu Arg Gly Pro Asp
 130 135 140
 Gly Met Ser Arg Gly Cys Ala Phe Val Thr Phe Thr Thr Arg Ser Met
 145 150 155 160
 Ala Gln Met Ala Ile Lys Ser Met His Gln Ala Gln Thr Met Glu Gly
 165 170 175
 Cys Ser Ser Pro Ile Val Val Lys Phe Ala Asp Thr Gln Lys Asp Lys
 180 185 190
 Glu Gln Lys Arg Met Thr Gln Gln Leu Gln Gln Gln Met Gln Gln Leu
 195 200 205
 Asn Ala Ala Ser Met Trp Gly Asn Leu Thr Gly Leu Asn Ser Leu Ala
 210 215 220
 Pro Gln Tyr Leu Ala Leu Leu Gln Gln Thr Ala Ser Ser Gly Asn Leu
 225 230 235 240
 Asn Ser Leu Ser Gly Leu His Pro Met Gly Ala Glu Tyr Gly Thr Gly
 245 250 255
 Met Thr Ser Gly Leu Asn Ala Ile Gln Leu Gln Asn Leu Ala Ala Leu
 260 265 270

Ala Ala Ala Ala Ser Ala Ala Gln Asn Thr Pro Ser Ala Gly Ala Ala
275 280 285

Leu Thr Ser Ser Ser Ser Pro Leu Ser Ile Leu Thr Ser Ser Gly Ser
290 295 300

Ser Pro Ser Ser Asn Asn Ser Ser Ile Asn Thr Met Ala Ser Leu Gly
305 310 315 320

Ala Leu Gln Thr Leu Ala Gly Ala Thr Ala Gly Leu Asn Val Asn Ser
325 330 335

Leu Ala Gly Met Ala Ala Phe Asn Gly Gly Leu Gly Ser Ser Leu Ser
340 345 350

Asn Gly Thr Gly Ser Thr Met Glu Ala Leu Ser Gln Ala Tyr Ser Gly
355 360 365

Ile Gln Gln Tyr Ala Ala Ala Ala Leu Pro Ser Leu Tyr Asn Gln Ser
370 375 380

Leu Leu Ser Gln Gln Gly Leu Gly Ala Ala Gly Ser Gln Lys Glu Gly
385 390 395 400

Pro Glu Gly Ala Asn Leu Phe Ile Tyr His Leu Pro Gln Glu Phe Gly
405 410 415

Asp Gln Asp Leu Leu Gln Met Phe Met Pro Phe Gly Asn Val Val Ser
420 425 430

Ser Lys Val Phe Ile Asp Lys Gln Thr Asn Leu Ser Lys Cys Phe Gly
435 440 445

Phe Val Ser Tyr Asp Asn Pro Val Ser Ala Gln Ala Ala Ile Gln Ser
450 455 460

Met Asn Gly Phe Gln Ile Gly Met Lys Arg Leu Lys Val Gln Leu Lys
465 470 475 480

Arg Ser Lys Asn Asp Ser Lys Pro Tyr
485

<210> 10

<211> 1470

<212> DNA

<213> *Xenopus laevis*

<400> 10

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gccgtctatg aaattaatgt tctccgagac agaagccaga atcctcctca gagcaaagga 180
tgctgtttta ttactttcta cacaagaaaa gctgcgtttag aagcacagaa tgctttgcac 240
aacatgaaag ttctccctgg gatgcatcat ccaatacaga tgaagccagc cgacagtga 300
aagaataatg ctgtggaaga ccgaaagcta tttatcggaa tggtttccaa gaattgtaat 360
gagaatgata tccgggccat gttctctccg tttggacaga tagaggaatg tcgtatcctg 420
cgaggccctg atggaatgag cagaggatgt gcattcgtta cgtttacaac tagatccatg 480
gcacagatgg caatcaaadc catgcaccaa gcacaaacca tggagggtg ttcctcacca 540

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atagtggtaa agttcgcaga cactcagaaa gacaaagaac agaagcgcag gacgcagcaa 600
cttcagcagc aaatgcagca gctcaatgca gcctcaatgt ggggtaacct gactggactg 660
aacagcttgg caccaccagta tttagcactc ctccagcaga ccgcctcctc tgggaacctc 720
aactccctaa gtggtctcca ccctatggga gctgagtacg gcaactggaat gacatcaggg 780
cttaatgcca tacagttaca gaatttggca gctttagcgg ctgctgctag tgctgcgcag 840
aacaccccaa gtgcaggagc agcgctcact tcttcagca gccccctcag catcctaacc 900
agttccgggt cctccccag ttcaaataac tcatccatca acaccatggc atccctagga 960
gctctacaga cattggctgg ggccacagct ggtctcaatg tcaattcgct tgcaggatatg 1020
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gcccttagtc aagcttactc tgggattcag cagtatgctg ccgctgcact tccttcactc 1140
tataaccaga gccttttgtc acaacagggt ttgggggctg cggggagtc gaaagaaggc 1200
ccagaaggag ccaacctttt tatataccac ctaccccagg agtttgggga ccaggatctc 1260
ctgcagatgt tcatgccatt tggaaatgtt gtgtcctcca aagttttcat cgacaaacaa 1320
acgaacctca gcaaattgtt tggcttcgta agttacgaca atcccgtttc tgctcagggt 1380
gctatccagt ccatgaacgg ctttcagatc ggaatgaaac gcctgaaagt ccaactcaaa 1440
cgctccaaga atgacagcaa accctactga                                     1470

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<210> 11

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 11

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala

1

5

<210> 12

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 12

atgctagcgt aaagttcgca gacactcaga aag

33

<210> 13

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 13

atgcggccgc tgcattgagc tgctgcattt gc

32

<210> 14
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 14
 atgctagcgt aaaatttgct gatacacaga ag 32

<210> 15
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 15
 atgcggccgc tgcgctgatt tgctgcatct gc 32

<210> 16
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 16
 taccatacgt atgttccaga ttacgct 27

<210> 17
 <211> 10
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 poly-A tail

<400> 17
 aaaaaaaaaa 10